SEQUENCE LISTING

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<120> Trans-Sialidases obtained fromTyrpanosoma congolense

<130> NUT-047-WO

<150> DE 10258400.1
<151> 2002-12-13

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<170> PatentIn version 3.1

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agg gag gtt ata att ccg aat ggt cgt gtg gat gcc cac tac tcc cgc       96
Arg Glu Val Ile Ile Pro Asn Gly Arg Val Asp Ala His Tyr Ser Arg
            20                  25                  30

gtc gtt gat ccc act gtt gtt gcg aag ggt aat aac att tat gtt ctc      144
Val Val Asp Pro Thr Val Val Ala Lys Gly Asn Asn Ile Tyr Val Leu
        35                  40                  45

gtt ggg cgg tac aat gtc acg cgg ggc tac tgg cac aat agg aac aac      192
Val Gly Arg Tyr Asn Val Thr Arg Gly Tyr Trp His Asn Arg Asn Asn
    50                  55                  60

aag gct ggc ata gcc gat tgg gag ccc ttc gtg tac aag ggc acg gtg      240
Lys Ala Gly Ile Ala Asp Trp Glu Pro Phe Val Tyr Lys Gly Thr Val
65                  70                  75                  80

aac gtg ggc acg aag ggc aat gcc act gat gtg tcg atc agc tgg gag      288
Asn Val Gly Thr Lys Gly Asn Ala Thr Asp Val Ser Ile Ser Trp Glu
                85                  90                  95

agg act gca ctg aag tcg ctg tac aac ttc ccg gtt tcg gga agc cct      336
Arg Thr Ala Leu Lys Ser Leu Tyr Asn Phe Pro Val Ser Gly Ser Pro
            100                 105                 110

ggc acg cag ttc ctt gga ggg gct ggg ggt ggt gtt gta aca tcc aac      384
Gly Thr Gln Phe Leu Gly Gly Ala Gly Gly Gly Val Val Thr Ser Asn
        115                 120                 125
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ggg acg att gtg ctg cca gtg cag gca agg aac aag gcc aac cgt gtt      432
Gly Thr Ile Val Leu Pro Val Gln Ala Arg Asn Lys Ala Asn Arg Val
    130                 135                 140

gtg agc atg atc ctg tac tcg gct gac gat gga aag tca tgg cac ttt      480
Val Ser Met Ile Leu Tyr Ser Ala Asp Asp Gly Lys Ser Trp His Phe
145                 150                 155                 160

ggg aag ggt gag gcc ggt gta ggc acg tcc gag gct gcc ctc act gag      528
Gly Lys Gly Glu Ala Gly Val Gly Thr Ser Glu Ala Ala Leu Thr Glu
                165                 170                 175

tgg gac ggc aag ctg ctg att agt gca cga tcc gat ggt gga cag ggc      576
Trp Asp Gly Lys Leu Leu Ile Ser Ala Arg Ser Asp Gly Gly Gln Gly
            180                 185                 190

tac cgc atg ata ttc gaa tcg agt gac ctt ggt gcg acg tgg aaa gag      624
Tyr Arg Met Ile Phe Glu Ser Ser Asp Leu Gly Ala Thr Trp Lys Glu
        195                 200                 205

atg ctc aac agc atc tcc cgc gtg att ggc aac tct ccg ggt cgc agt      672
Met Leu Asn Ser Ile Ser Arg Val Ile Gly Asn Ser Pro Gly Arg Ser
    210                 215                 220

ggt cct ggc agc tcg agt ggc ttc atc acg gtg aca gtg gag ggt gtg      720
Gly Pro Gly Ser Ser Ser Gly Phe Ile Thr Val Thr Val Glu Gly Val
225                 230                 235                 240

cct gtg atg ctg att acc cac ccg aag aac ctt aag ggc tcg tat tat      768
Pro Val Met Leu Ile Thr His Pro Lys Asn Leu Lys Gly Ser Tyr Tyr
                245                 250                 255

cgg gac cgt ctg cag ctg tgg atg acg gac ggc aat cgt atg tgg cat      816
Arg Asp Arg Leu Gln Leu Trp Met Thr Asp Gly Asn Arg Met Trp His
            260                 265                 270

gtc ggg cag gtc tct gag ggc gac gat aac agc gct tac agc tcc ctg      864
Val Gly Gln Val Ser Glu Gly Asp Asp Asn Ser Ala Tyr Ser Ser Leu
        275                 280                 285

ctg tac act ccg gac ggg gtc ctg tac tgc ttg cat gag cag aac att      912
Leu Tyr Thr Pro Asp Gly Val Leu Tyr Cys Leu His Glu Gln Asn Ile
    290                 295                 300

gat gag gtg tac agc ctc cac ctt gtg cgc ctt gtg gac gag ctg aaa      960
Asp Glu Val Tyr Ser Leu His Leu Val Arg Leu Val Asp Glu Leu Lys
305                 310                 315                 320

agc att aaa tca acg gct ctg gtg tgg aag gca cag gac gag ctt ctc     1008
Ser Ile Lys Ser Thr Ala Leu Val Trp Lys Ala Gln Asp Glu Leu Leu
                325                 330                 335

ctg ggc aac tgc ctc ccg ggc gat aaa tac gat ccc ggg tgt gac ggc     1056
Leu Gly Asn Cys Leu Pro Gly Asp Lys Tyr Asp Pro Gly Cys Asp Gly
            340                 345                 350

atc ccc acc gct ggg ctt gcc ggg ctg ctg gta gga ccc ctg acg gag     1104
Ile Pro Thr Ala Gly Leu Ala Gly Leu Leu Val Gly Pro Leu Thr Glu
        355                 360                 365

aag acg tgg ccc gac gcg tat cgg tgc gtg aac gct gca acc agc ggc     1152
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    370                 375                 380

gct gtg agc act gct gaa ggc gtg cgg ctg gac gtg ggt ggc ggt ggc     1200
Ala Val Ser Thr Ala Glu Gly Val Arg Leu Asp Val Gly Gly Gly Gly
385                 390                 395                 400

cat gtt gtg tgg ccc gtg agt gag cag ggg cag gac cag cgg tat tac     1248
His Val Val Trp Pro Val Ser Glu Gln Gly Gln Asp Gln Arg Tyr Tyr
                405                 410                 415

ttt acc aac agc gag ttc acg ctc gcc gtc acg gtg cgg ttt gac gag     1296
Phe Thr Asn Ser Glu Phe Thr Leu Ala Val Thr Val Arg Phe Asp Glu
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atg cca cgg ggg gag ctc ccg ttg ctg ggg ttt gtg aac cgc aaa ggg     1344
Met Pro Arg Gly Glu Leu Pro Leu Leu Gly Phe Val Asn Arg Lys Gly
        435                 440                 445

aag gtg aag aag ata ctg aag gtg tcg ctg agc ggg gtg gag tgg ctc     1392
Lys Val Lys Lys Ile Leu Lys Val Ser Leu Ser Gly Val Glu Trp Leu
    450                 455                 460

ctg gca tac ggg aat gag tac aac agc aca gcc gct gag ccg ctg gac     1440
Leu Ala Tyr Gly Asn Glu Tyr Asn Ser Thr Ala Ala Glu Pro Leu Asp
465                 470                 475                 480

gtg aac gag agc cac cag gtg gtg cta gcg ctt cac gac ggg atc gtc     1488
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Ser
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            20                  25                  30

Val Val Asp Pro Thr Val Val Ala Lys Gly Asn Asn Ile Tyr Val Leu
        35                  40                  45

Val Gly Arg Tyr Asn Val Thr Arg Gly Tyr Trp His Asn Arg Asn Asn
    50                  55                  60

Lys Ala Gly Ile Ala Asp Trp Glu Pro Phe Val Tyr Lys Gly Thr Val
65                  70                  75                  80

Asn Val Gly Thr Lys Gly Asn Ala Thr Asp Val Ser Ile Ser Trp Glu
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85 90 95

Arg Thr Ala Leu Lys Ser Leu Tyr Asn Phe Pro Val Ser Gly Ser Pro
100 105 110

Gly Thr Gln Phe Leu Gly Gly Ala Gly Gly Gly Val Val Thr Ser Asn
115 120 125

Gly Thr Ile Val Leu Pro Val Gln Ala Arg Asn Lys Ala Asn Arg Val
130 135 140

Val Ser Met Ile Leu Tyr Ser Ala Asp Asp Gly Lys Ser Trp His Phe
145 150 155 160

Gly Lys Gly Glu Ala Gly Val Gly Thr Ser Glu Ala Ala Leu Thr Glu
165 170 175

Trp Asp Gly Lys Leu Leu Ile Ser Ala Arg Ser Asp Gly Gly Gln Gly
180 185 190

Tyr Arg Met Ile Phe Glu Ser Ser Asp Leu Gly Ala Thr Trp Lys Glu
195 200 205

Met Leu Asn Ser Ile Ser Arg Val Ile Gly Asn Ser Pro Gly Arg Ser
210 215 220

Gly Pro Gly Ser Ser Ser Gly Phe Ile Thr Val Thr Val Glu Gly Val
225 230 235 240

Pro Val Met Leu Ile Thr His Pro Lys Asn Leu Lys Gly Ser Tyr Tyr
245 250 255

Arg Asp Arg Leu Gln Leu Trp Met Thr Asp Gly Asn Arg Met Trp His
260 265 270

Val Gly Gln Val Ser Glu Gly Asp Asp Asn Ser Ala Tyr Ser Ser Leu
275 280 285

Leu Tyr Thr Pro Asp Gly Val Leu Tyr Cys Leu His Glu Gln Asn Ile
290 295 300

Asp Glu Val Tyr Ser Leu His Leu Val Arg Leu Val Asp Glu Leu Lys
305 310 315 320

Ser Ile Lys Ser Thr Ala Leu Val Trp Lys Ala Gln Asp Glu Leu Leu
325 330 335

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Leu Gly Asn Cys Leu Pro Gly Asp Lys Tyr Asp Pro Gly Cys Asp Gly
            340                 345                 350

Ile Pro Thr Ala Gly Leu Ala Gly Leu Leu Val Gly Pro Leu Thr Glu
        355                 360                 365

Lys Thr Trp Pro Asp Ala Tyr Arg Cys Val Asn Ala Ala Thr Ser Gly
    370                 375                 380

Ala Val Ser Thr Ala Glu Gly Val Arg Leu Asp Val Gly Gly Gly Gly
385                 390                 395                 400

His Val Val Trp Pro Val Ser Glu Gln Gly Gln Asp Gln Arg Tyr Tyr
                405                 410                 415

Phe Thr Asn Ser Glu Phe Thr Leu Ala Val Thr Val Arg Phe Asp Glu
            420                 425                 430

Met Pro Arg Gly Glu Leu Pro Leu Leu Gly Phe Val Asn Arg Lys Gly
        435                 440                 445

Lys Val Lys Lys Ile Leu Lys Val Ser Leu Ser Gly Val Glu Trp Leu
    450                 455                 460

Leu Ala Tyr Gly Asn Glu Tyr Asn Ser Thr Ala Ala Glu Pro Leu Asp
465                 470                 475                 480

Val Asn Glu Ser His Gln Val Val Leu Ala Leu His Asp Gly Ile Val
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Ser
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1               5                   10                  15

ttc gat aca cgt tat ctt cgc gct tcc gac agc agt ctc ata gac aca       96
Phe Asp Thr Arg Tyr Leu Arg Ala Ser Asp Ser Ser Leu Ile Asp Thr
            20                  25                  30
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gct atg aaa tac agt gcc gat cag ggg aag acg tgg aaa act gaa atc      144
Ala Met Lys Tyr Ser Ala Asp Gln Gly Lys Thr Trp Lys Thr Glu Ile
        35                  40                  45

ata ata aaa aat gct aga cta act gat aac ttt tcc cgc gtc gtt gat      192
Ile Ile Lys Asn Ala Arg Leu Thr Asp Asn Phe Ser Arg Val Val Asp
    50                  55                  60

cca acg gtt gtt gtt aag ggt gat aac ttg ttt att ttt gtt ggg agg      240
Pro Thr Val Val Val Lys Gly Asp Asn Leu Phe Ile Phe Val Gly Arg
65                  70                  75                  80

tac aac acc tca tct gcc cca tgg gtc tgg cag gaa aac ggt aaa gac      288
Tyr Asn Thr Ser Ser Ala Pro Trp Val Trp Gln Glu Asn Gly Lys Asp
                85                  90                  95

tgg gat gta ctg ttg tac aag gcc aag gtg agg aag gaa tca gcg ggt      336
Trp Asp Val Leu Leu Tyr Lys Ala Lys Val Arg Lys Glu Ser Ala Gly
            100                 105                 110

ggg gta cca tca gtg agc ttt aca tgg gac gaa ccc cta tac ctg aag      384
Gly Val Pro Ser Val Ser Phe Thr Trp Asp Glu Pro Leu Tyr Leu Lys
        115                 120                 125

cat ctg ctc acc tct gtc ggt aaa ata gac ggc agg tcc ctc ata caa      432
His Leu Leu Thr Ser Val Gly Lys Ile Asp Gly Arg Ser Leu Ile Gln
    130                 135                 140

tac att ggt ggc gtt gga aat ggt att gta aca ccg aaa ggt act atc      480
Tyr Ile Gly Gly Val Gly Asn Gly Ile Val Thr Pro Lys Gly Thr Ile
145                 150                 155                 160

gtg ttt cca gtt cag gtt tta aac acc aac aaa tcc gtc atg aac atg      528
Val Phe Pro Val Gln Val Leu Asn Thr Asn Lys Ser Val Met Asn Met
                165                 170                 175

ctt ctg tat tca agt aac gac gga aaa acc tgg gag ttc agc aaa act      576
Leu Leu Tyr Ser Ser Asn Asp Gly Lys Thr Trp Glu Phe Ser Lys Thr
            180                 185                 190

tcc aca ccc gcg ggc aca act gag gcc tcc ctt gtt tgg tgg gat gga      624
Ser Thr Pro Ala Gly Thr Thr Glu Ala Ser Leu Val Trp Trp Asp Gly
        195                 200                 205

caa cta ctt ctc aca agc aga aca act ccg gat gtc ggc agc cgc aaa      672
Gln Leu Leu Leu Thr Ser Arg Thr Thr Pro Asp Val Gly Ser Arg Lys
    210                 215                 220

gta tat tta aca agc gac ctc gga act tca tgg aat gaa gcg atc gga      720
Val Tyr Leu Thr Ser Asp Leu Gly Thr Ser Trp Asn Glu Ala Ile Gly
225                 230                 235                 240

agt atc tct cgt gta att ggt aac tcg cgg tac cgt aac gat cct ggg      768
Ser Ile Ser Arg Val Ile Gly Asn Ser Arg Tyr Arg Asn Asp Pro Gly
                245                 250                 255

ggg tca ggt agc tca att gcc ata act gtg gag gga gta ccg gtg atg      816
Gly Ser Gly Ser Ser Ile Ala Ile Thr Val Glu Gly Val Pro Val Met
            260                 265                 270

ctg att acc cac ccg                                                 831
Leu Ile Thr His Pro
        275
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<213> Trypanosoma congolense

<400> 4

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Phe Asp Thr Arg Tyr Leu Arg Ala Ser Asp Ser Ser Leu Ile Asp Thr
            20                  25                  30

Ala Met Lys Tyr Ser Ala Asp Gln Gly Lys Thr Trp Lys Thr Glu Ile
        35                  40                  45

Ile Ile Lys Asn Ala Arg Leu Thr Asp Asn Phe Ser Arg Val Val Asp
    50                  55                  60

Pro Thr Val Val Val Lys Gly Asp Asn Leu Phe Ile Phe Val Gly Arg
65                  70                  75                  80

Tyr Asn Thr Ser Ser Ala Pro Trp Val Trp Gln Glu Asn Gly Lys Asp
                85                  90                  95

Trp Asp Val Leu Leu Tyr Lys Ala Lys Val Arg Lys Glu Ser Ala Gly
            100                 105                 110

Gly Val Pro Ser Val Ser Phe Thr Trp Asp Glu Pro Leu Tyr Leu Lys
        115                 120                 125

His Leu Leu Thr Ser Val Gly Lys Ile Asp Gly Arg Ser Leu Ile Gln
    130                 135                 140

Tyr Ile Gly Gly Val Gly Asn Gly Ile Val Thr Pro Lys Gly Thr Ile
145                 150                 155                 160

Val Phe Pro Val Gln Val Leu Asn Thr Asn Lys Ser Val Met Asn Met
                165                 170                 175

Leu Leu Tyr Ser Ser Asn Asp Gly Lys Thr Trp Glu Phe Ser Lys Thr
            180                 185                 190

Ser Thr Pro Ala Gly Thr Thr Glu Ala Ser Leu Val Trp Trp Asp Gly
        195                 200                 205

Gln Leu Leu Leu Thr Ser Arg Thr Thr Pro Asp Val Gly Ser Arg Lys
    210                 215                 220
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Val Tyr Leu Thr Ser Asp Leu Gly Thr Ser Trp Asn Glu Ala Ile Gly
225 230 235 240

Ser Ile Ser Arg Val Ile Gly Asn Ser Arg Tyr Arg Asn Asp Pro Gly
245 250 255

Gly Ser Gly Ser Ser Ile Ala Ile Thr Val Glu Gly Val Pro Val Met
260 265 270

Leu Ile Thr His Pro
275